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- Search numbers may not be continuous; all searches are represented.
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Search	Most Recent Queries	Time	Result
#11	Search **#9 AND #10**	14:55:54	14
#10	Search **osteopontin** Field: **All Fields**	14:55:44	2408
#9	Search **weber** Field: **Author**	14:55:19	21652
#2	Search **OPN-c**	14:55:03	2
#5	Search **(breast) AND ("SPP-1" [TIAB] OR "SPP 1" [TIAB] OR "SPP1" [TIAB] OR "secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)" [TIAB] OR "secreted-phosphoprotein-1-(osteopontin,-bone-sialoprotein-I,-early-T-lymphocyte-activation-1)" [TIAB] OR "secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T lymphocyte activation 1)" [TIAB] OR "BSPI" [TIAB] OR "ETA-1" [TIAB] OR "ETA 1" [TIAB] OR "OPN" [TIAB] OR "Bone sialoprotein 1" [TIAB] OR "Bone-sialoprotein-1" [TIAB] OR "Urinary stone protein" [TIAB] OR "Urinary-stone-protein" [TIAB] OR "SPP-1" [TIAB] OR "SPP 1" [TIAB] OR "Nephropontin" [TIAB] OR "Uropontin" [TIAB] OR "BNSP" [TIAB] OR "Secreted phosphoprotein 1" [TIAB] OR "Secreted-phosphoprotein-1" [TIAB])**	14:54:10	51
#3	**Related Articles** for **PubMed** (Select **12181091**)	12:49:45	192
#1	Search **OPN**	12:47:31	827

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DATE: Monday, May 09, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ	
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☐	L23	L22 and l17	16
☐	L22	l3.ti.	30
☐	L21	20030124128.pn.	1
☐	L20	20030087250.pn.	1
☐	L19	L18 not @ay>2002	72
☐	L18	L17 and L16	123
☐	L17	cancer$ or neoplas$ or tumor$	162015
☐	L16	L15 or L14	320
☐	L15	L5.clm.	251
☐	L14	L5.ab.	129
☐	L13	L3.ab.	64
☐	L12	L11 and L6	0
☐	L11	L5 and L10	894
☐	L10	L9 or L8 or L7	59922
☐	L9	(536/23.1)![CCLS]	11747
☐	L8	(530/350)![CCLS]	16729
☐	L7	(435/4 |435/6 |435/7.1 |435/7.23 |435/7.92 |435/7.94)![CCLS]	42303
☐	L6	L5 and L2	4
☐	L5	L4 or L3	3142
☐	L4	OPN$	1427
☐	L3	osteopontin	1850
☐	L2	weber.in.	14421
☐	L1	wber.in.	0

END OF SEARCH HISTORY

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                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:         May  4, 2005, 19:25:36 ; Search time 3779 Seconds
                                          (without alignments)
                                          11039.942 Million cell updates/sec

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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                14:  gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                 SUMMARIES
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                                 ALIGNMENTS


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ACCESSION   D28761
VERSION     D28761.1  GI:633076
KEYWORDS    .
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REFERENCE   1  (bases 1 to 861)
  AUTHORS   Saitoh,Y., Kuratsu,J., Takeshima,H., Yamamoto,S. and Ushio,Y.
  TITLE     Expression of osteopontin in human glioma. Its correlation with
the
            malignancy
  JOURNAL   Lab. Invest. 72 (1), 55-63 (1995)
  MEDLINE   95139605
   PUBMED   7837791
REFERENCE   2  (bases 1 to 861)
  AUTHORS   Saitoh,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-1994) Yoshiki Saitoh, Kumamoto University
Medical
            School, Department of Neurosurgery; 1-1-1 Honjo, Kumamoto,
Kumamoto
            860, Japan (Tel:81-96-344-2111(ex.5684), Fax:81-96-371-8064)
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HITSHMESEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQLDDQSAEAHSHKQSRL

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ORIGIN

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0;

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Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
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Qy         121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
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Qy         841 AGTGCATCTTCTGAGGTCAAT 861
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Db         841 AGTGCATCTTCTGAGGTCAAT 861
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                         GenCore version 5.1.6
                Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          May  4, 2005, 09:10:38 ; Search time 535 Seconds
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      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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                              ALIGNMENTS


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DT   11-DEC-2002  (first entry)
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DE   cDNA encoding human ovarian cancer marker OV50.
XX
KW   Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW   central nervous system disorder; bacterial meningitis; viral meningitis;
KW   Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW   brain herniation; inflammation; encephalitis; testicular disorder;
KW   nontuberculous granulomatous orchitis; connective tissue disorder;
KW   heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW   histological type; carcinogenic; ovarian cancer marker; gene; ss.
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PN   WO200271928-A2.
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PD   19-SEP-2002.
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PR   10-AUG-2001; 2001US-0311732P.
PR   19-SEP-2001; 2001US-0323580P.
PR   26-SEP-2001; 2001US-0324967P.
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PR   26-SEP-2001; 2001US-0325149P.
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PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Monahan JE,  Gannavarapu M,  Hoersch S,  Kamatkar S,  Kovatis SG;
PI   Meyers RE,  Morrisey MP,  Olandt PJ,  Sen A,  Vieby PO,  Mills GB;
PI   Bast RC,  Lu K,  Schmandt RE,  Zhao X,  Glatt K;
XX
DR   WPI; 2002-723277/78.
DR   P-PSDB; ABG96388.
XX
PT   Assessing whether a patient is afflicted with ovarian cancer, useful in
PT   assessing the stage or progression of the disease, comprises comparing
PT   the expression level of a cancer marker in a sample from a patient and
PT   from a non cancer patient.
XX
PS   Disclosure; Page 357; 481pp; English.
XX
CC   The present invention relates to a new method for assessing whether a
CC   patient is afflicted with ovarian cancer. The method involves comparing
CC   the expression level of a marker in a patient sample and the normal level
CC   of expression of the marker in a control non-ovarian cancer sample, where
CC   the marker is selected from 363 cancer markers described in the
CC   specification. The method of the invention is useful in diagnosing or
CC   characterising cancer, in detecting the presence of cancer as early as
CC   possible, and the recurrence of ovarian cancer. The method may also be of
CC   particular use with patients having an enhanced risk of developing
CC   ovarian cancer (e.g. patients having a familial history of ovarian
CC   cancer). The cancer markers may be used in the management and treatment
CC   of e.g. brain and central nervous system disorders (e.g. bacterial and
CC   viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC   disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC   inflammations (e.g. bacterial or viral meningitis or encephalitis),
CC   testicular disorders (e.g. nontuberculous granulomatous orchitis),
CC   connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC   disease or atherosclerosis). The compositions and methods may also be
CC   used in assessing the histological type of neoplasm associated with
CC   ovarian cancer, monitoring the progression of ovarian cancer, determining
CC   whether ovarian cancer has metastasized or is likely to metastasize,
CC   selecting a composition for inhibiting ovarian cancer, assessing the
CC   ovarian carcinogenic potential of a compound, or inhibiting ovarian
CC   cancer or at risk of developing ovarian cancer. The present nucleic acid
CC   sequence encodes one of the ovarian cancer markers described in the
CC   invention
XX
SQ   Sequence 861 BP; 261 A; 193 C; 204 G; 203 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 861;  DB 6;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-244;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
```

```
Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861

RESULT 2
ACC50249
ID   ACC50249 standard; cDNA; 861 BP.
XX
AC   ACC50249;
```

```
XX
DT   12-JUN-2003  (first entry)
XX
DE   Breast cancer associated cDNA sequence SEQ ID NO:339.
XX
KW   Human; breast cancer; cytostatic; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003004989-A2.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US019669.
XX
PR   21-JUN-2001; 2001US-0299887P.
PR   27-JUN-2001; 2001US-0301572P.
PR   18-JUL-2001; 2001US-0306501P.
PR   25-SEP-2001; 2001US-0325002P.
PR   05-MAR-2002; 2002US-0362585P.
PR   14-MAY-2002; 2002US-0380391P.
XX
PA   (MILL-) MILLENIUM PHARM INC.
XX
PI   Lillie J,  Gannavarapu M,  Glatt K,  Hoersh S,  Kamatkar S;
PI   Mertens M,  Monahan JE,  Myer V,  Wang Y,  Xu Y,  Zhao X,  Meyers RE;
PI   Bast RC,  Hortobagyi GN,  Pusztai L,  Meric F,  Sahin A,  Mills GB;
XX
DR   WPI; 2003-210381/20.
DR   P-PSDB; ABR47551.
XX
PT   Breast cancer diagnosis or treatment by comparing the level of expression
PT   of a marker in a patient sample with that in the control non-breast
PT   cancer sample.
XX
PS   Claim 1; SEQ ID NO 339; 128pp; English.
XX
CC   The present invention describes a method for assessing whether a patient
CC   is afflicted with breast cancer. The method comprises comparing the level
CC   of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC   ABR47386 to ABR47632) in a patient sample and the normal level of
CC   expression of the marker in a control non-breast cancer sample, where a
CC   significant increase in the level of expression of the marker in the
CC   patient sample and the normal level is an indication that the patient is
CC   afflicted with breast cancer. The breast cancer associated sequences from
CC   the present invention have cytostatic activities and can be used in gene
CC   therapy. The method is useful for diagnosing and treating breast cancer.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 861 BP; 261 A; 193 C; 204 G; 203 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 861;  DB 8;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-244;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861

RESULT 3
ACF12916
ID   ACF12916 standard; cDNA; 861 BP.
XX
AC   ACF12916;
XX
DT   10-SEP-2003  (first entry)
XX
```

```
DE   Human cervical cancer cell marker encoding cDNA SEQ ID NO:175.
XX
KW   Human; cervical cancer; cervical cancer marker; cancer therapy;
KW   detection; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2002101075-A2.
XX
PD   19-DEC-2002.
XX
PF   12-JUN-2002; 2002WO-US018638.
XX
PR   13-JUN-2001; 2001US-0298155P.
PR   13-JUN-2001; 2001US-0298159P.
PR   14-NOV-2001; 2001US-0335936P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R,  Chen Y,  Zhao X,  Monahan JE,  Kamatkar S;
PI   Gannavarapu M,  Glatt K,  Hoersch S;
XX
DR   WPI; 2003-156967/15.
DR   P-PSDB; ABR92133.
XX
PT   New isolated nucleic acid molecule useful for detecting, characterizing,
PT   preventing and treating human cervical cancers, in various prognostic and
PT   diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
PS   Claim 4; Page 336; 386pp; English.
XX
CC   ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC   given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC   normal indicates the presence of cervical cancer. Also described: (1) a
CC   vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC   assessing (M1) whether a patient is afflicted with cervical cancer,
CC   comprising comparing the level of expression of a marker in a patient's
CC   sample, and the normal level of expression of the marker in a control non
CC   -cervical cancer sample, where a significant increase in the level of
CC   expression of the marker in the patient's sample relative to that in the
CC   control sample is an indication that the patient is afflicted with
CC   cervical cancer. (I) has cytostatic activity, and can be used in gene
CC   therapy and in vaccines. (I) is useful in detecting, characterising,
CC   preventing and treating human cervical cancers. (I) may also be used in
CC   various prognostic and diagnostic assays, pharmacogenomics and in
CC   monitoring clinical trials
XX
SQ   Sequence 861 BP; 261 A; 193 C; 204 G; 203 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 861;  DB 8;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-244;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861


RESULT 4
ADB75482
ID   ADB75482 standard; cDNA; 861 BP.
XX
AC   ADB75482;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Prostate cancer marker cDNA.
XX
KW   Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO2003009814-A2.
XX
PD   06-FEB-2003.
XX
PF   25-JUL-2002; 2002WO-US023913.
XX
PR   25-JUL-2001; 2001US-0307982P.
PR   22-AUG-2001; 2001US-0314356P.
PR   25-SEP-2001; 2001US-0325020P.
PR   12-DEC-2001; 2001US-0341746P.
PR   05-MAR-2002; 2002US-0362158P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R,  Monahan JE,  Endege WO,  Gannavarapu M,  Gorbatcheva B;
PI   Hoersh S,  Kamatkar S,  Wonsey AM,  Glatt K,  Zhao X,  Anderson D;
XX
DR   WPI; 2003-248033/24.
XX
PT   New nucleic acid molecule, useful for diagnosing or treating prostate
PT   cancer.
XX
PS   Disclosure; SEQ ID NO 306; 99pp; English.
XX
CC   The invention relates to newly discovered cancer markers associated with
CC   the cancerous state of prostate cells. Also disclosed is a method of
CC   assessing whether a patient is afflicted with prostate cancer. The method
CC   of the invention involves assessing whether a patient is afflicted with
CC   prostate cancer by comparing the level of expression of a marker in a
CC   patient sample and the normal level of expression of the marker in a
CC   control non-prostate cancer sample, where a significant increase in the
CC   level of expression of the marker in the patient sample and the normal
CC   level indicates that the patient is afflicted with prostate cancer.
CC   Nucleic acids of the invention are useful for diagnosing or treating
CC   prostate cancer, and may be useful in gene therapy. Sequences given in
CC   ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 861 BP; 261 A; 193 C; 204 G; 203 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 861;  DB 10;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-244;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
```

```
Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
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RESULT 5
ADQ88469
ID   ADQ88469 standard; DNA; 861 BP.
XX
AC   ADQ88469;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human OPN-a isoform, osteopontin-c (OPN-c) DNA.
XX
KW   Tumour; OPN-b; osteopontin-b; OPN-c; osteopontin-c; carcinoma; sarcoma;
KW   leukaemia; lymphoma; prostate gland tumour; colon tumour; lung tumour;
KW   breast tumour; stomach tumour; bladder tumour; ovary tumour;
KW   thyroid gland tumour; pancreas tumour; liver tumour; glioma; therapy;
KW   human; osteopontin-a; OPN-a; gene; ds.
XX
OS   Homo sapiens.
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XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "Human OPN-a isoform, osteopontin-c (OPN-c)
FT                   protein"
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PN   US2004142865-A1.
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PD   22-JUL-2004.
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PF   02-OCT-2003; 2003US-00678355.
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PR   02-OCT-2002; 2002US-0415712P.
XX
PA   (WEBE/) WEBER G F.
XX
PI   Weber GF;
XX
DR   WPI; 2004-533520/51.
DR   P-PSDB; ADQ88475.
DR   GENBANK; D28761.
XX
PT   Treating patient having tumor, or is at risk of developing a tumor e.g.,
PT   sarcoma, carcinoma, leukemia, involves administering an agent that
PT   inhibits expression or activity of osteopontin-b or osteopontin-c, to the
PT   patient.
XX
PS   Claim 5; SEQ ID NO 5; 21pp; English.
XX
CC   The present invention relates to a method of treating a patient who has a
CC   tumour or who is at risk of developing a tumour. The method involves
CC   administering to the patient an agent that inhibits the expression or
CC   activity of at least one of osteopontin-b or osteopontin-c (OPN-b or OPN-
CC   c). The invention is useful for treating tumour such as carcinoma,
CC   sarcoma, leukaemia or lymphoma and tumour of the prostate gland, colon,
CC   lung, breast, stomach, bladder, ovary, thyroid gland, pancreas or liver
CC   and preferably for treating a patient having glioma. The present sequence
CC   is human osteopontin-a (OPN-a) isoform, OPN-c DNA.
XX
SQ   Sequence 861 BP; 261 A; 193 C; 204 G; 203 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 861;  DB 13;  Length 861;
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                         GenCore version 5.1.6
                  Copyright (c) 1993 - 2005  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          May  5, 2005, 02:55:48 ; Search time 194 Seconds
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Total number of hits satisfying chosen parameters:      2405568

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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
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; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4492
;   LENGTH: 1509
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-4492

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                        GenCore version 5.1.6
                Copyright (c) 1993 - 2005  Compugen Ltd.

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Run on:         May  5, 2005, 05:07:26 ; Search time 5671 Seconds
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  5     861  100.0     861  15  US-10-301-822-146           Sequence 146, App
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 18     772   89.7    1524  14  US-10-097-340-228           Sequence 228, App
 19     772   89.7    1524  14  US-10-171-311-173           Sequence 173, App
 20     772   89.7    1524  15  US-10-205-823-304           Sequence 304, App
 21     772   89.7    1524  15  US-10-177-293-337           Sequence 337, App
 22     772   89.7    1524  15  US-10-301-822-144           Sequence 144, App
 23     772   89.7    1524  16  US-10-269-909-70            Sequence 70, Appl
 24     772   89.7    1524  17  US-10-170-385-268           Sequence 268, App
 25     772   89.7    1524  17  US-10-295-027-507           Sequence 507, App
 26     772   89.7    1524  17  US-10-295-027-1116          Sequence 1116, Ap
 27     772   89.7    1524  17  US-10-087-080-11            Sequence 11, Appl
 28     772   89.7    1524  17  US-10-240-425-392           Sequence 392, App
 29     772   89.7    1524  17  US-10-229-345-6             Sequence 6, Appli
 30     772   89.7    1524  17  US-10-274-177-6             Sequence 6, Appli
 31     772   89.7    1524  18  US-10-717-597-279           Sequence 279, App
 32     772   89.7    1524  18  US-10-650-112-6             Sequence 6, Appli
 33     772   89.7    1524  18  US-10-764-649-7             Sequence 7, Appli
 34     772   89.7    1524  18  US-10-734-564-8             Sequence 8, Appli
 35     772   89.7    1524  18  US-10-775-920-208           Sequence 208, App
 36     772   89.7    1524  19  US-10-278-698-282           Sequence 282, App
 37     772   89.7    1524  19  US-10-278-698-796           Sequence 796, App
 38     772   89.7    1524  19  US-10-818-066-1             Sequence 1, Appli
 39     772   89.7    1549  18  US-10-775-920-215           Sequence 215, App
 40     772   89.7    1734  18  US-10-723-860-7782          Sequence 7782, Ap
 41     772   89.7    2209  14  US-10-198-846-13927         Sequence 13927, A
 42     771   89.5     942  14  US-10-097-340-226           Sequence 226, App
 43     771   89.5     942  14  US-10-171-311-171           Sequence 171, App
 44     771   89.5     942  15  US-10-205-823-302           Sequence 302, App
 45     771   89.5     942  15  US-10-177-293-335           Sequence 335, App


                                  ALIGNMENTS


RESULT 1
US-10-097-340-230
; Sequence 230, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
;  APPLICANT: John MONAHAN
;  APPLICANT:  Manjula GANNAVARAPU
;  APPLICANT:  Sebastian HOERSCH
;  APPLICANT:  Shubhangi KAMATKAR
;  APPLICANT:  Steve G. KOVATS
;  APPLICANT:  Rachel E. MEYERS
;  APPLICANT:  Michael MORRISEY
;  APPLICANT:  Peter OLANDT
;  APPLICANT:  Ami SEN
;  APPLICANT:  Peter VEIBY
;  APPLICANT:  Gordon B. MILLS
;  APPLICANT:  Robert C. BAST, Jr.
;  APPLICANT:  Karen LU
;  APPLICANT:  Rosemarie SCHMANDT
;  APPLICANT:  Xumei ZHAO
;  APPLICANT:  Karen GLATT
;  TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
;  TITLE OF INVENTION:  Assessment, Prevention, and Therapy of Ovarian Cancer
;  FILE REFERENCE: MRI-030
;  CURRENT APPLICATION NUMBER: US/10/097,340
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: 60/276,025
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/325,149
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/276,026
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/324,967
;  PRIOR FILING DATE: 2001/09/26
;  PRIOR APPLICATION NUMBER: 60/311,732
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/325,102
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/323,580
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 363
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-097-340-230

  Query Match             100.0%;  Score 861;  DB 14;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy          841 AGTGCATCTTCTGAGGTCAAT 861
                |||||||||||||||||||||
Db          841 AGTGCATCTTCTGAGGTCAAT 861


RESULT 2
US-10-171-311-175
; Sequence 175, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-171-311-175

  Query Match             100.0%;  Score 861;  DB 14;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861


RESULT 3
US-10-205-823-306
; Sequence 306, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Monahan, John E.
;  APPLICANT:  Endege, Wilson O.
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Gorbatcheva, Bella
;  APPLICANT:  Hoersch, Sebastian
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Wonsey, Angela M.
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Anderson, Dustin
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;  TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF PROSTATE CANCER
;  FILE REFERENCE: MRI-044
;  CURRENT APPLICATION NUMBER: US/10/205,823
;  CURRENT FILING DATE:  2002-07-25
;  PRIOR APPLICATION NUMBER: 60/307,982
;  PRIOR FILING DATE: 2001-07-25
;  PRIOR APPLICATION NUMBER: 60/314,356
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/325,020
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: 60/341,746
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: 60/362,158
;  PRIOR FILING DATE: 2002-03-05
;  NUMBER OF SEQ ID NOS: 455
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 306
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-205-823-306

  Query Match             100.0%;  Score 861;  DB 15;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
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Qy          181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy          241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy          301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy          361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy          841 AGTGCATCTTCTGAGGTCAAT 861
                |||||||||||||||||||||
Db          841 AGTGCATCTTCTGAGGTCAAT 861

RESULT 4
US-10-177-293-339
; Sequence 339, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Gannavarpu, Manjula
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Mertens, Maureen
;  APPLICANT:  Myer, Vic
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Hoersch, Sebastian
;  APPLICANT:  Monahan, John
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Bast Jr., Robert C.
;  APPLICANT:  Hortobagyi, Gabriel N.
;  APPLICANT:  Pusztai, Lajos
;  APPLICANT:  Meric, Funda
;  APPLICANT:  Sahin, Aysegul
;  APPLICANT:  Mills, Gordon B.
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
ASSESSMENT,
;  TITLE OF INVENTION:  PREVENTION, AND THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-038
;  CURRENT APPLICATION NUMBER: US/10/177,293
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: US 60/299,887
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: US 60/301,572
;  PRIOR FILING DATE: 2001-06-27
;  PRIOR APPLICATION NUMBER: US 60/306,501
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/325,002
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/362,585
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US 60/xxx,xxx
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 506
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 339
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-177-293-339

  Query Match             100.0%;  Score 861;  DB 15;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
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Qy          361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy          841 AGTGCATCTTCTGAGGTCAAT 861
                |||||||||||||||||||||
Db          841 AGTGCATCTTCTGAGGTCAAT 861


RESULT 5
US-10-301-822-146
; Sequence 146, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Berger, Allison
;  APPLICANT:  Guillemette, Tracy L.
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Schlegel, Robert
;  APPLICANT:  Monahan, John E.
;  APPLICANT:  Thibodeau, Stephen N.
;  APPLICANT:  Burgart, Lawrence J.
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;  TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF COLON CANCER
;  FILE REFERENCE: MPM01-029P2RNM
;  CURRENT APPLICATION NUMBER: US/10/301,822
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 60/339,971
;  PRIOR FILING DATE: 2001-12-10
;  PRIOR APPLICATION NUMBER: US 60/361,978
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US 60/381,988
;  PRIOR FILING DATE: 2002-05-20
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(861)
US-10-301-822-146

  Query Match             100.0%;  Score 861;  DB 15;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
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Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861


RESULT 6
US-10-678-355-5
; Sequence 5, Application US/10678355
; Publication No. US20040142865A1
; GENERAL INFORMATION:
;  APPLICANT: Weber, Georg F.
;  TITLE OF INVENTION: OSTEOPONTIN-BASED CANCER THERAPIES
;  FILE REFERENCE: 00398-148001
;  CURRENT APPLICATION NUMBER: US/10/678,355
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: US 60/415,712
;  PRIOR FILING DATE: 2002-10-02
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-678-355-5

  Query Match             100.0%;  Score 861;  DB 18;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861


RESULT 7
US-10-775-920-217
; Sequence 217, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
;  APPLICANT: Mergen Ltd
;  TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED
POLYPEPTIDES
;  TITLE OF INVENTION:  OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS
OVEREXPRESSED
;  TITLE OF INVENTION:  IN CERTAIN CANCERS
;  FILE REFERENCE: Mergen - 0010B
;  CURRENT APPLICATION NUMBER: US/10/775,920
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: US 60/447,900
;  PRIOR FILING DATE: 2003-02-13
;  NUMBER OF SEQ ID NOS: 385
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-775-920-217

  Query Match             100.0%;  Score 861;  DB 18;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420

Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600

Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780

Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy        841 AGTGCATCTTCTGAGGTCAAT 861
              |||||||||||||||||||||
Db        841 AGTGCATCTTCTGAGGTCAAT 861
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                        GenCore version 5.1.6
              Copyright (c) 1993 - 2005  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          May  5, 2005, 02:15:58 ; Search time 3114 Seconds
                                            (without alignments)
                                            10524.514 Million cell updates/sec

Title:           US-10-678-355-5
Perfect score:   861
Sequence:        1 atgagaattgcagtgatttg..........gtgcatcttctgaggtcaat 861

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:      68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                1:  gb_est1:*
                2:  gb_est2:*
                3:  gb_htc:*
                4:  gb_est3:*
                5:  gb_est4:*
                6:  gb_est5:*
                7:  gb_est6:*
                8:  gb_gss1:*
                9:  gb_gss2:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
                 %
Result          Query
  No.   Score   Match  Length DB  ID                          Description
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     1  856.2    99.4    1349  3  CR617515                    CR617515 full-leng
     2  846.6    98.3    1060  5  BX379560                    BX379560 BX379560
     3  826.8    96.0    1070  1  AL546356                    AL546356 AL546356
     4    772    89.7    1137  1  AL542602                    AL542602 AL542602
     5    772    89.7    1341  3  CR610632                    CR610632 full-leng
     6    772    89.7    1360  3  CR617116                    CR617116 full-leng
     7    772    89.7    1361  3  CR615698                    CR615698 full-leng
     8    772    89.7    1372  3  CR594254                    CR594254 full-leng
  9      772    89.7   1372  3  CR604739                     CR604739 full-leng
 10      772    89.7   1383  3  CR593792                     CR593792 full-leng
 11      772    89.7   1391  3  CR612712                     CR612712 full-leng
 12      772    89.7   1393  3  CR607920                     CR607920 full-leng
 13      772    89.7   1398  3  CR608709                     CR608709 full-leng
 14      772    89.7   1411  3  CR615383                     CR615383 full-leng
 15      772    89.7   1413  3  CR593987                     CR593987 full-leng
 16      772    89.7   1415  3  CR624945                     CR624945 full-leng
 17      772    89.7   1421  3  CR594667                     CR594667 full-leng
 18      772    89.7   1422  3  CR618369                     CR618369 full-leng
 19      772    89.7   1422  3  CR622075                     CR622075 full-leng
 20      772    89.7   1470  3  CR625747                     CR625747 full-leng
 21      772    89.7   1474  3  CR614191                     CR614191 full-leng
 22      772    89.7   1502  3  CR606646                     CR606646 full-leng
 23      772    89.7   1565  3  CR602900                     CR602900 full-leng
 24    771.6    89.6    993  5  BX397759                     BX397759 BX397759
 25    766.2    89.0    945  9  AY417969                     AY417969 Homo sapi
 26    766.2    89.0   1145  5  BX438909                     BX438909 BX438909
 27    766.2    89.0   1214  3  CR624176                     CR624176 full-leng
 28    766.2    89.0   1406  3  CR609665                     CR609665 full-leng
 29    766.2    89.0   1417  3  CR603247                     CR603247 full-leng
 30    766.2    89.0   1419  3  CR590765                     CR590765 full-leng
 31    766.2    89.0   1423  3  CR596445                     CR596445 full-leng
 32    766.2    89.0   1424  3  CR605902                     CR605902 full-leng
 33    766.2    89.0   1426  3  CR591447                     CR591447 full-leng
 34    766.2    89.0   1426  3  CR613613                     CR613613 full-leng
 35    766.2    89.0   1427  3  CR596475                     CR596475 full-leng
 36    766.2    89.0   1428  3  CR591466                     CR591466 full-leng
 37    766.2    89.0   1435  3  CR618220                     CR618220 full-leng
 38    766.2    89.0   1437  3  CR601143                     CR601143 full-leng
 39    766.2    89.0   1439  3  CR599125                     CR599125 full-leng
 40    766.2    89.0   1440  3  CR610252                     CR610252 full-leng
 41    766.2    89.0   1440  3  CR626471                     CR626471 full-leng
 42    766.2    89.0   1442  3  CR600714                     CR600714 full-leng
 43    766.2    89.0   1443  3  CR616615                     CR616615 full-leng
 44    766.2    89.0   1446  3  CR600744                     CR600744 full-leng
 45    766.2    89.0   1448  3  CR619881                     CR619881 full-leng


                               ALIGNMENTS


RESULT 1
CR617515
LOCUS       CR617515                1349 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI031YL18 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR617515
VERSION     CR617515.1  GI:50498322
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1349)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1349)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1349
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI031YL18"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.4%;  Score 856.2;  DB 3;  Length 1349;
  Best Local Similarity   99.7%;  Pred. No. 1.8e-235;
  Matches  858;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 144

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 204

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 264

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 324

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 384

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 444

Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 504
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Qy          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
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Db          505 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 564

Qy          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
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Db          565 GACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 624

Qy          541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          625 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 684

Qy          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
                ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          685 AGTCAGCTGGATGACCAGAGTGCTGAAACCCACAGCCACAAGCAGTCCAGATTATATAAG 744

Qy          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
                |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          745 CGGAAAGCCAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 804

Qy          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          805 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 864

Qy          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
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Db          865 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 924

Qy          841 AGTGCATCTTCTGAGGTCAAT 861
                |||||||||||||||||||||
Db          925 AGTGCATCTTCTGAGGTCAAT 945
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                     GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         May  5, 2005, 05:07:26 ; Search time 5671 Seconds
                                           (without alignments)
                                          928.345 Million cell updates/sec

Title:          US-10-678-355-5
Perfect score:  861
Sequence:       1 atgagaattgcagtgatttg..........gtgcatcttctgaggtcaat 861

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters:      11308400

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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                2:  /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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      Pred. No. is the number of results predicted by chance to have a
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      and is derived by analysis of the total score distribution.

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Result          Query
   No.   Score  Match Length DB  ID                          Description
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     1     861  100.0    861  14  US-10-097-340-230            Sequence 230, App
   2      861  100.0     861  14  US-10-171-311-175            Sequence 175, App
   3      861  100.0     861  15  US-10-205-823-306            Sequence 306, App
   4      861  100.0     861  15  US-10-177-293-339            Sequence 339, App
   5      861  100.0     861  15  US-10-301-822-146            Sequence 146, App
   6      861  100.0     861  18  US-10-678-355-5              Sequence 5, Appli
   7      861  100.0     861  18  US-10-775-920-217            Sequence 217, App
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   9    778.4   90.4     900  18  US-10-775-920-218            Sequence 218, App
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  12      772   89.7    1447  18  US-10-775-169-221            Sequence 221, App
  13      772   89.7    1447  18  US-10-775-920-209            Sequence 209, App
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  15      772   89.7    1469  19  US-10-690-880-9              Sequence 9, Appli
  16      772   89.7    1486  18  US-10-775-920-210            Sequence 210, App
  17      772   89.7    1520  18  US-10-775-920-207            Sequence 207, App
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  19      772   89.7    1524  14  US-10-171-311-173            Sequence 173, App
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  21      772   89.7    1524  15  US-10-177-293-337            Sequence 337, App
  22      772   89.7    1524  15  US-10-301-822-144            Sequence 144, App
  23      772   89.7    1524  16  US-10-269-909-70             Sequence 70, Appl
  24      772   89.7    1524  17  US-10-170-385-268            Sequence 268, App
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  26      772   89.7    1524  17  US-10-295-027-1116           Sequence 1116, Ap
  27      772   89.7    1524  17  US-10-087-080-11             Sequence 11, Appl
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  29      772   89.7    1524  17  US-10-229-345-6              Sequence 6, Appli
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  33      772   89.7    1524  18  US-10-764-649-7              Sequence 7, Appli
  34      772   89.7    1524  18  US-10-734-564-8              Sequence 8, Appli
  35      772   89.7    1524  18  US-10-775-920-208            Sequence 208, App
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  38      772   89.7    1524  19  US-10-818-066-1              Sequence 1, Appli
  39      772   89.7    1549  18  US-10-775-920-215            Sequence 215, App
  40      772   89.7    1734  18  US-10-723-860-7782           Sequence 7782, Ap
  41      772   89.7    2209  14  US-10-198-846-13927          Sequence 13927, A
  42      771   89.5     942  14  US-10-097-340-226            Sequence 226, App
  43      771   89.5     942  14  US-10-171-311-171            Sequence 171, App
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  45      771   89.5     942  15  US-10-177-293-335            Sequence 335, App


RESULT 4
US-10-177-293-339
; Sequence 339, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Gannavarpu, Manjula
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Mertens, Maureen
;  APPLICANT:  Myer, Vic
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Hoersch, Sebastian
;  APPLICANT:  Monahan, John
; APPLICANT:  Meyers, Rachel E.
; APPLICANT:  Bast Jr., Robert C.
; APPLICANT:  Hortobagyi, Gabriel N.
; APPLICANT:  Pusztai, Lajos
; APPLICANT:  Meric, Funda
; APPLICANT:  Sahin, Aysegul
; APPLICANT:  Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
ASSESSMENT,
; TITLE OF INVENTION:  PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE:  2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 339
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-177-293-339

  Query Match             100.0%;  Score 861;  DB 15;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
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Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
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Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180

Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
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Db        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240

Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
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Db        421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480

Qy        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
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Db        481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540

Qy        541 GCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACAGTTATGAAACG 600
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Qy        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy        661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
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Qy        721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
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Db        841 AGTGCATCTTCTGAGGTCAAT 861
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                       GenCore version 5.1.6
                Copyright (c) 1993 - 2005  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         May  5, 2005, 05:07:26 ; Search time 5671 Seconds
                                           (without alignments)
                                           928.345 Million cell updates/sec

Title:          US-10-678-355-5
Perfect score:  861
Sequence:       1 atgagaattgcagtgatttg..........gtgcatcttctgaggtcaat 861

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters:      11308400

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                18:  /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                19:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                20:  /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                21:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                22:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                             SUMMARIES
                 %
Result           Query
  No.   Score    Match Length DB  ID                          Description
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     1     861   100.0    861  14  US-10-097-340-230            Sequence 230, App
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   2     861   100.0      861  14  US-10-171-311-175           Sequence 175, App
   3     861   100.0      861  15  US-10-205-823-306           Sequence 306, App
   4     861   100.0      861  15  US-10-177-293-339           Sequence 339, App
   5     861   100.0      861  15  US-10-301-822-146           Sequence 146, App
   6     861   100.0      861  18  US-10-678-355-5             Sequence 5, Appli
   7     861   100.0      861  18  US-10-775-920-217           Sequence 217, App
   8   778.4    90.4      900  18  US-10-678-355-3             Sequence 3, Appli
   9   778.4    90.4      900  18  US-10-775-920-218           Sequence 218, App
  10     772    89.7     1447  17  US-10-240-425-1270          Sequence 1270, Ap
  11     772    89.7     1447  18  US-10-717-597-188           Sequence 188, App
  12     772    89.7     1447  18  US-10-775-169-221           Sequence 221, App
  13     772    89.7     1447  18  US-10-775-920-209           Sequence 209, App
  14     772    89.7     1469  9  US-09-919-770-1             Sequence 1, Appli
  15     772    89.7     1469  19  US-10-690-880-9             Sequence 9, Appli
  16     772    89.7     1486  18  US-10-775-920-210           Sequence 210, App
  17     772    89.7     1520  18  US-10-775-920-207           Sequence 207, App
  18     772    89.7     1524  14  US-10-097-340-228           Sequence 228, App
  19     772    89.7     1524  14  US-10-171-311-173           Sequence 173, App
  20     772    89.7     1524  15  US-10-205-823-304           Sequence 304, App
  21     772    89.7     1524  15  US-10-177-293-337           Sequence 337, App
  22     772    89.7     1524  15  US-10-301-822-144           Sequence 144, App
  23     772    89.7     1524  16  US-10-269-909-70            Sequence 70, Appl
  24     772    89.7     1524  17  US-10-170-385-268           Sequence 268, App
  25     772    89.7     1524  17  US-10-295-027-507           Sequence 507, App
  26     772    89.7     1524  17  US-10-295-027-1116          Sequence 1116, Ap
  27     772    89.7     1524  17  US-10-087-080-11            Sequence 11, Appl
  28     772    89.7     1524  17  US-10-240-425-392           Sequence 392, App
  29     772    89.7     1524  17  US-10-229-345-6             Sequence 6, Appli
  30     772    89.7     1524  17  US-10-274-177-6             Sequence 6, Appli
  31     772    89.7     1524  18  US-10-717-597-279           Sequence 279, App
  32     772    89.7     1524  18  US-10-650-112-6             Sequence 6, Appli
  33     772    89.7     1524  18  US-10-764-649-7             Sequence 7, Appli
  34     772    89.7     1524  18  US-10-734-564-8             Sequence 8, Appli
  35     772    89.7     1524  18  US-10-775-920-208           Sequence 208, App
  36     772    89.7     1524  19  US-10-278-698-282           Sequence 282, App
  37     772    89.7     1524  19  US-10-278-698-796           Sequence 796, App
  38     772    89.7     1524  19  US-10-818-066-1             Sequence 1, Appli
  39     772    89.7     1549  18  US-10-775-920-215           Sequence 215, App
  40     772    89.7     1734  18  US-10-723-860-7782          Sequence 7782, Ap
  41     772    89.7     2209  14  US-10-198-846-13927         Sequence 13927, A
  42     771    89.5      942  14  US-10-097-340-226           Sequence 226, App
  43     771    89.5      942  14  US-10-171-311-171           Sequence 171, App
  44     771    89.5      942  15  US-10-205-823-302           Sequence 302, App
  45     771    89.5      942  15  US-10-177-293-335           Sequence 335, App


                               ALIGNMENTS


RESULT 1
US-10-097-340-230
; Sequence 230, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
;  APPLICANT: John MONAHAN
;  APPLICANT:  Manjula GANNAVARAPU
;  APPLICANT:  Sebastian HOERSCH
;  APPLICANT:  Shubhangi KAMATKAR
;  APPLICANT:  Steve G. KOVATS
;  APPLICANT:  Rachel E. MEYERS
;  APPLICANT:  Michael MORRISEY
;  APPLICANT:  Peter OLANDT
;  APPLICANT:  Ami SEN
;  APPLICANT:  Peter VEIBY
;  APPLICANT:  Gordon B. MILLS
;  APPLICANT:  Robert C. BAST, Jr.
;  APPLICANT:  Karen LU
;  APPLICANT:  Rosemarie SCHMANDT
;  APPLICANT:  Xumei ZHAO
;  APPLICANT:  Karen GLATT
;  TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
;  TITLE OF INVENTION:  Assessment, Prevention, and Therapy of Ovarian Cancer
;  FILE REFERENCE: MRI-030
;  CURRENT APPLICATION NUMBER: US/10/097,340
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: 60/276,025
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/325,149
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/276,026 ⇒ ON50 , page 14.
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/324,967
;  PRIOR FILING DATE: 2001/09/26
;  PRIOR APPLICATION NUMBER: 60/311,732
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/325,102
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/323,580
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 363
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-097-340-230

  Query Match             100.0%;  Score 861;  DB 14;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-255;
  Matches  861;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGAATTGCAGTGATTTGCTTTTGCCTCCTAGGCATCACCTGTGCCATACCAGTTAAA 60

Qy         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCTGATTCTGGAAGTTCTGAGGAAAAGCAGAATGCTGTGTCCTCTGAAGAAACCAAT 120

Qy        121 GACTTTAAACAAGAGACCCTTCCAAGTAAGTCCAACGAAAGCCATGACCACATGGATGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 ATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGACTCGAACGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTGATGATGTAGATGACACTGATGATTCTCACCAGTCTGATGAGTCTCACCATTCTGAT 300

Qy        301 GAATCTGATGAACTGGTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 CCAGTTGTCCCCACAGTAGACACATATGATGGCCGAGGTGATAGTGTGGTTTATGGACTG 420
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Qy          421 AGGTCAAAATCTAAGAAGTTTCGCAGACCTGACATCCAGTACCCTGATGCTACAGACGAG 480
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Qy          481 CACATCACCTCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGTT 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AGTCAGCTGGATGACCAGAGTGCTGAAGCCCACAGCCACAAGCAGTCCAGATTATATAAG 660

Qy          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 CGGAAAGCTAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCC 720

Qy          721 AAAGTCAGCCGTGAATTCCACAGCCATGAATTTCACAGCCATGAAGATATGCTGGTTGTA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840
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Db          781 GACCCCAAAAGTAAGGAAGAAGATAAACACCTGAAATTTCGTATTTCTCATGAATTAGAT 840

Qy          841 AGTGCATCTTCTGAGGTCAAT 861
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Db          841 AGTGCATCTTCTGAGGTCAAT 861
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